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RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/954,556

DATE: 10/09/2001  
 TIME: 08:54:19

Input Set : A:\RTS-0250\_Seq\_ASCII.txt  
 Output Set: N:\CRF3\10092001\I954556.raw

3 <110> APPLICANT: Brett P. Monia  
 4 Susan M. Freier  
 5 Scott Cooper  
 7 <120> TITLE OF INVENTION: ANTISENSE MODULATION OF FIBROBLAST GROWTH FACTOR RECEPTOR 2

EXPRESSION

9 <130> FILE REFERENCE: RTS-0250

C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/954,556

C--> 11 <141> CURRENT FILING DATE: 2001-09-14

11 <160> NUMBER OF SEQ ID NOS: 108

14 <210> SEQ ID NO: 1

15 <211> LENGTH: 20

16 <212> TYPE: DNA

17 <213> ORGANISM: Artificial Sequence

19 <220> FEATURE:

21 <223> OTHER INFORMATION: Antisense Oligonucleotide

23 <400> SEQUENCE: 1

24 tccgtcatcg ctccctcaggg

27 <210> SEQ ID NO: 2

28 <211> LENGTH: 20

29 <212> TYPE: DNA

30 <213> ORGANISM: Artificial Sequence

32 <220> FEATURE:

34 <223> OTHER INFORMATION: Antisense Oligonucleotide

36 <400> SEQUENCE: 2

37 atgcattctg cccccaagga

40 <210> SEQ ID NO: 3

41 <211> LENGTH: 4268

42 <212> TYPE: DNA

43 <213> ORGANISM: Homo sapiens

45 <220> FEATURE:

47 <220> FEATURE:

48 <221> NAME/KEY: CDS

49 <222> LOCATION: (274)...(2739)

51 <400> SEQUENCE: 3

52 cccaaggacc actcttctgc gtttgagtt gctcccaca accccgggct cgtcgtttc 60

54 tccatcccga cccacgcggg gcgcggggac aacacaggtc gcggaggagc gttgccattc 120

56 aagtgactgc agcagcagcg gcagcgctc ggttcctgag cccaccgcag gctgaaggca 180

58 ttgcgcgtag tccatgcccg tagagggaagt gtgcagatgg gattaacgtc cacatggaga 240

60 tatggaagag gaccggggat tggtaaccgta acc atg gtc agc tgg ggt cgt ttc 294

61 Met Val Ser Trp Gly Arg Phe

62 1 5

64 atc tgc ctg gtc gtg gtc acc atg gca acc ttg tcc ctg gcc cgg ccc 342

65 Ile Cys Leu Val Val Val Thr Met Ala Thr Leu Ser Leu Ala Arg Pro

66 10 15 20

68 tcc ttc agt tta gtt gag gat acc aca tta gag cca gaa gag cca cca 390

69 Ser Phe Ser Leu Val Glu Asp Thr Thr Leu Glu Pro Glu Glu Pro Pro

70 25 30 35

72 acc aaa tac caa atc tct caa cca gaa gtg tac gtg gct gcg cca ggg 438

ENTERED

20

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73 Thr Lys Tyr Gln Ile Ser Gln Pro Glu Val Tyr Val Ala Ala Pro Gly
74 40 45 50 55
76 gag tcg cta gag gtg cgc tgc ctg ttg aaa gat gcc gcc gtg atc agt 486
77 Glu Ser Leu Glu Val Arg Cys Leu Leu Lys Asp Ala Ala Val Ile Ser
78 60 65 70
80 tgg act aag gat ggg gtg cac ttg ggg ccc aac aat agg aca gtg ctt 534
81 Trp Thr Lys Asp Gly Val His Leu Gly Pro Asn Asn Arg Thr Val Leu
82 75 80 85
84 att ggg gag tac ttg cag ata aag ggc gcc acg cct aga gac tcc ggc 582
85 Ile Gly Glu Tyr Leu Gln Ile Lys Gly Ala Thr Pro Arg Asp Ser Gly
86 90 95 100
88 ctc tat gct tgt act gcc agt agg act gta gac agt gaa act tgg tac 630
89 Leu Tyr Ala Cys Thr Ala Ser Arg Thr Val Asp Ser Glu Thr Trp Tyr
90 105 110 115
92 ttc atg gtg aat gtc aca gat gcc atc tca tcc gga gat gat gag gat 678
93 Phe Met Val Asn Val Thr Asp Ala Ile Ser Ser Gly Asp Asp Glu Asp
94 120 125 130 135
96 gac acc gat ggt gcg gaa gat ttt gtc agt gag aac agt aac aac aag 726
97 Asp Thr Asp Gly Ala Glu Asp Phe Val Ser Glu Asn Ser Asn Asn Lys
98 140 145 150
100 aga gca cca tac tgg acc aac aca gaa aag atg gaa aag cgg ctc cat 774
101 Arg Ala Pro Tyr Trp Thr Asn Thr Glu Lys Met Glu Lys Arg Leu His
102 155 160 165
104 gct gtg cct gcg gcc aac act gtc aag ttt cgc tgc cca gcc ggg ggg 822
105 Ala Val Pro Ala Ala Asn Thr Val Lys Phe Arg Cys Pro Ala Gly Gly
106 170 175 180
108 aac cca atg cca acc atg cgg tgg ctg aaa aac ggg aag gag ttt aag 870
109 Asn Pro Met Pro Thr Met Arg Trp Leu Lys Asn Gly Lys Glu Phe Lys
110 185 190 195
112 cag gag cat cgc att gga ggc tac aag gta cga aac cag cac tgg agc 918
113 Gln Glu His Arg Ile Gly Gly Tyr Lys Val Arg Asn Gln His Trp Ser
114 200 205 210 215
116 ctc att atg gaa agt gtg gtc cca tct gac aag gga aat tat acc tgt 966
117 Leu Ile Met Glu Ser Val Val Pro Ser Asp Lys Gly Asn Tyr Thr Cys
118 220 225 230
120 gtg gtg gag aat gaa tac ggg tcc atc aat cac acg tac cac ctg gat 1014
121 Val Val Glu Asn Glu Tyr Gly Ser Ile Asn His Thr Tyr His Leu Asp
122 235 240 245
124 gtt gtg gag cga tcg cct cac cgg ccc atc ctc caa gcc gga ctg ccg 1062
125 Val Val Glu Arg Ser Pro His Arg Pro Ile Leu Gln Ala Gly Leu Pro
126 250 255 260
128 gca aat gcc tcc aca gtg gtc gga gga gac gta gag ttt gtc tgc aag 1110
129 Ala Asn Ala Ser Thr Val Val Gly Gly Asp Val Glu Phe Val Cys Lys
130 265 270 275
132 gtt tac agt gat gcc cag ccc cac atc cag tgg atc aag cac gtg gaa 1158
133 Val Tyr Ser Asp Ala Gln Pro His Ile Gln Trp Ile Lys His Val Glu
134 280 285 290 295
136 aag aac ggc agt aaa tac ggg ccc gac ggg ctg ccc tac ctc aag gtt 1206
137 Lys Asn Gly Ser Lys Tyr Gly Pro Asp Gly Leu Pro Tyr Leu Lys Val

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Input Set : A:\RTS-0250\_Seq\_ASCII.txt

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```

204 tct aaa ggc aac ctc cga gaa tac ctc cga gcc cgg agg cca ccc ggg      2022
205 Ser Lys Gly Asn Leu Arg Glu Tyr Leu Arg Ala Arg Pro Pro Gly
206          570          575          580
208 atg gag tac tcc tat gac att aac cgt gtt cct gag gag cag atg acc      2070
209 Met Glu Tyr Ser Tyr Asp Ile Asn Arg Val Pro Glu Glu Gln Met Thr
210          585          590          595
212 ttc aag gac ttg gtg tca tgc acc tac cag ctg gcc aga ggc atg gag      2118
213 Phe Lys Asp Leu Val Ser Cys Thr Tyr Gln Leu Ala Arg Gly Met Glu
214 600          605          610          615
216 tac ttg gct tcc caa aaa tgt att cat cga gat tta gca gcc aga aat      2166
217 Tyr Leu Ala Ser Gln Lys Cys Ile His Arg Asp Leu Ala Ala Arg Asn
218          620          625          630
220 gtt ttg gta aca gaa aac aat gtg atg aaa ata gca gac ttt gga ctc      2214
221 Val Leu Val Thr Glu Asn Asn Val Met Lys Ile Ala Asp Phe Gly Leu
222          635          640          645
224 gcc aga gat atc aac aat ata gac tat tac aaa aag acc acc aat ggg      2262
225 Ala Arg Asp Ile Asn Asn Ile Asp Tyr Tyr Lys Lys Thr Thr Asn Gly
226          650          655          660
228 cgg ctt cca gtc aag tgg atg gct cca gaa gcc ctg ttt gat aga gta      2310
229 Arg Leu Pro Val Lys Trp Met Ala Pro Glu Ala Leu Phe Asp Arg Val
230          665          670          675
232 tac act cat cag agt gat gtc tgg tcc ttc ggg gtg tta atg tgg gag      2358
233 Tyr Thr His Gln Ser Asp Val Trp Ser Phe Gly Val Leu Met Trp Glu
234 680          685          690          695
236 atc ttc act tta ggg ggc tcg ccc tac cca ggg att ccc gtg gag gaa      2406
237 Ile Phe Thr Leu Gly Gly Ser Pro Tyr Pro Gly Ile Pro Val Glu Glu
238          700          705          710
240 ctt ttt aag ctg ctg aag gaa gga cac aga atg gat aag cca gcc aac      2454
241 Leu Phe Lys Leu Leu Lys Glu Gly His Arg Met Asp Lys Pro Ala Asn
242          715          720          725
244 tgc acc aac gaa ctg tac atg atg atg agg gac tgt tgg cat gca gtg      2502
245 Cys Thr Asn Glu Leu Tyr Met Met Met Arg Asp Cys Trp His Ala Val
246          730          735          740
248 ccc tcc cag aga cca acg ttc aag cag ttg gta gaa gac ttg gat cga      2550
249 Pro Ser Gln Arg Pro Thr Phe Lys Gln Leu Val Glu Asp Leu Asp Arg
250          745          750          755
252 att ctc act ctc aca acc aat gag gaa tac ttg gac ctc agc caa cct      2598
253 Ile Leu Thr Leu Thr Thr Asn Glu Glu Tyr Leu Asp Leu Ser Gln Pro
254 760          765          770          775
256 ctc gaa cag tat tca cct agt tac cct gac aca aga agt tct tgt tct      2646
257 Leu Glu Gln Tyr Ser Pro Ser Tyr Pro Asp Thr Arg Ser Ser Cys Ser
258          780          785          790
260 tca gga gat gat tct gtt ttt tct cca gac ccc atg cct tac gaa cca      2694
261 Ser Gly Asp Asp Ser Val Phe Ser Pro Asp Pro Met Pro Tyr Glu Pro
262          795          800          805
264 tgc ctt cct cag tat cca cac ata aac ggc agt gtt aaa aca tga      2739
265 Cys Leu Pro Gln Tyr Pro His Ile Asn Gly Ser Val Lys Thr
266          810          815          820
268 atgactgtgt ctgcctgtcc ccaaacagga cagcactggg aacctagcta cactgagcag      2799

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270 ggagaccatg cctcccagag cttgttgtct ccacttgtat atatggatca gaggagtaaa 2859
272 taattggaaa agtaatcagc atatgtgtaa agatttatac agttgaaaac ttgtaatctt 2919
274 ccccaggagg agaagaaggt ttctggagca gtggactgcc acaagccacc atgtaacccc 2979
276 tctcacctgc cgtgcgttct ggcgtggac cagtaggact caagggtggac gtgcgttctg 3039
278 ccttccctgt taattttgta ataattggag aagatttatg tcagcacaca cttacagagc 3099
280 acaaatgcag tatatagggt ctggatgtat gtaaatatat tcaaattatg tataaatata 3159
282 tattatatat ttacaaggag ttattttttg tattgatttt aaatggatgt cccaatgcac 3219
284 ctagaaaatt ggtctctctt tttttaatag ctatttgcta aatgctgttc ttacacataa 3279
286 tttcttaatt ttcaccgagc agagggtgaa aaatactttt gctttcaggg aaaatggtat 3339
288 aacgttaatt tattaataaa ttggtaatat acaaaaacaat taatcattta tagttttttt 3399
290 tgtaatttaa gtggcatttc tatgcaggca gcacagcaga ctagttaatc tattgcttgg 3459
292 acttaactag ttatcagatc ctttgaaaag agaataatta caatatatga ctaatttggg 3519
294 gaaaatgaag ttttgattta ttgtgtttta aatgctgctg tcagacgatt gttcttagac 3579
296 ctccataaag ccccatatta aaagaactca ttcataggaa ggtgtttcat tttggtgtgc 3639
298 aacctgttca ttacgtcaac gcaacgtcta actggacttc ccaagataaa tggtagcagc 3699
300 gtccctctaa aagatgcctt aatccattcc ttgaggacag accttagttg aaatgatagc 3759
302 agaattgtgt tctctctggc agctggcctt ctgcttctga gttgcacatt aatcagatta 3819
304 gcctgattct cttcagtgaa ttttgataat ggcttcagaa ctcttgcgtg tggagacgcc 3879
306 tgttaggatc ttcaagtcac atcatagaaa attgaaacac agagtgtgtc tgctgatagt 3939
308 tttggggata cgtccatctt ttttaagggt tgctttcatc taattctggc aggacctcac 3999
310 caaaagatcc agcctcatac ctacatcaga caaaatatcg ccggtgttcc ttctgtacta 4059
312 aagtattgtg ttttgcttgg gaaacaccca ctactttgc aatagccgtg caagatgaat 4119
314 gcagattaca ctgatcttat gtgttacaaa attggagaaa gtatttaata aaacctgtta 4179
316 atttttatac tgacaataaa aatgtttcta cagatattaa tgtaacaag acaaaataaa 4239
318 tgtcacgcaa cttaaaaaaa aaaaaaaaaa 4268
321 <210> SEQ ID NO: 4
322 <211> LENGTH: 22
323 <212> TYPE: DNA
324 <213> ORGANISM: Artificial Sequence
326 <220> FEATURE:
328 <223> OTHER INFORMATION: PCR Primer
330 <400> SEQUENCE: 4
331 aaggaccact cttctgcgtt tg 22
334 <210> SEQ ID NO: 5
335 <211> LENGTH: 19
336 <212> TYPE: DNA
337 <213> ORGANISM: Artificial Sequence
339 <220> FEATURE:
341 <223> OTHER INFORMATION: PCR Primer
343 <400> SEQUENCE: 5
344 tgggtcggga tggagaaag 19
347 <210> SEQ ID NO: 6
348 <211> LENGTH: 20
349 <212> TYPE: DNA
350 <213> ORGANISM: Artificial Sequence
352 <220> FEATURE:
354 <223> OTHER INFORMATION: PCR Probe
356 <400> SEQUENCE: 6
357 cccacaaccc cgggctcgtc 20

```

Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

## VERIFICATION SUMMARY

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Input Set : A:\RTS-0250\_Seq\_ASCII.txt

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L:11 M:270 C: Current Application Number differs, Replaced Current Application No  
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:1191 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17  
L:1192 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17  
L:1193 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17  
L:1603 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17  
L:1604 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17  
L:1605 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17  
L:5150 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29  
L:5413 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29